

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/572,189
Source: IFL0P
Date Processed by STIC: 04/06/2006

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

**FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT
MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221**

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. **EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)**
2. **U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450**
3. **Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314**

Revised 01/10/06

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 10/572, 189

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."

2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.

3 Misaligned Amino Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.

4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.

5 Variable Length Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.

6 PatentIn 2.0 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.

7 Skipped Sequences (OLD RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.

8 Skipped Sequences (NEW RULES) Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

9 Use of n's or Xaa's (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

10 Invalid <213> Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence. (see item 11 below)

11 Use of <220> Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section or use "chemically synthesized" as explanation. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32), also Sec. 1.823 of Sequence Rules

12 PatentIn 2.0 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.

13 Misuse of n/Xaa "n" can only represent a single nucleotide; "Xaa" can only represent a single amino acid



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/572,189

DATE: 04/06/2006
TIME: 10:45:48

Input Set : A:\Sequence Listing (13111-00033-US).txt
Output Set: N:\CRF4\04062006\J572189.raw

3 <110> APPLICANT: Ostermann, Kai
4 Rodel, Gerhard
6 <120> TITLE OF INVENTION: SECRETION OF PROTEINS FROM YEASTS
8 <130> FILE REFERENCE: 13111-00033-US
---> 10 <140> CURRENT APPLICATION NUMBER: US/10/572,189
---> 10 <141> CURRENT FILING DATE: 2006-03-15
10 <150> PRIOR APPLICATION NUMBER: PCT/EP2004/010346
11 <151> PRIOR FILING DATE: 2004-09-15
13 <150> PRIOR APPLICATION NUMBER: DE 103 42 794.5
14 <151> PRIOR FILING DATE: 2003-09-16
16 <160> NUMBER OF SEQ ID NOS: 56
18 <170> SOFTWARE: PatentIn version 3.3
20 <210> SEQ ID NO: 1
22 <211> LENGTH: 171
24 <212> TYPE: DNA
26 <213> ORGANISM: Schizosaccharomyces pombe
29 <220> FEATURE:
31 <221> NAME/KEY: CDS
33 <222> LOCATION: (1)..(171)
35 <400> SEQUENCE: 1
36 atg aag atc acc gct gtc att gcc ctt tta ttc tca ctt gct gct gcc 48
37 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
38 1 5 10 15
40 tca cct att cca gtt gcc gat cct ggt gtg gtt tca gtt agc aag tca 96
41 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
42 20 25 30
44 tat gct gat ttc ctt cgt gtt tac caa agt tgg aac act ttt gct aat 144
45 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
46 35 40 45
48 cct gat aga ccc aac ttg aaa aag cgc 171
49 Pro Asp Arg Pro Asn Leu Lys Lys Arg
50 50 55
53 <210> SEQ ID NO: 2
55 <211> LENGTH: 57
57 <212> TYPE: PRT
59 <213> ORGANISM: Schizosaccharomyces pombe
62 <400> SEQUENCE: 2
64 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
65 1 5 10 15
68 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
69 20 25 30
72 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
73 35 40 45

Does Not Comply
Corrected Diskette Needed

(Pj-5)

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/572,189

DATE: 04/06/2006
TIME: 10:45:48

Input Set : A:\Sequence Listing (13111-00033-US).txt
Output Set: N:\CRF4\04062006\J572189.raw

76 Pro Asp Arg Pro Asn Leu Lys Lys Arg
77 50 55
80 <210> SEQ ID NO: 3
82 <211> LENGTH: 60
84 <212> TYPE: DNA
86 <213> ORGANISM: Schizosaccharomyces pombe
90 <220> FEATURE:
92 <221> NAME/KEY: CDS
94 <222> LOCATION: (1)..(60)
97 <220> FEATURE:
99 <221> NAME/KEY: sig_peptide
101 <222> LOCATION: (1)..(60)
105 <400> SEQUENCE: 3
106 atg aag atc acc gct gtc att gcc ctt tta ttc tca ctt gct gct gcc 48
107 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
108 1 5 10 15
110 tca cct att cca 60
111 Ser Pro Ile Pro
112 20
115 <210> SEQ ID NO: 4
117 <211> LENGTH: 20
119 <212> TYPE: PRT
121 <213> ORGANISM: Schizosaccharomyces pombe
124 <400> SEQUENCE: 4
126 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
127 1 5 10 15
130 Ser Pro Ile Pro
131 20
134 <210> SEQ ID NO: 5
136 <211> LENGTH: 81
138 <212> TYPE: DNA
140 <213> ORGANISM: Schizosaccharomyces pombe
143 <220> FEATURE:
145 <221> NAME/KEY: CDS
147 <222> LOCATION: (1)..(81)
150 <400> SEQUENCE: 5
151 aag tca tat gct gat ttc ctt cgt gtt tac caa agt tgg aac act ttt 48
152 Lys Ser Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe
153 1 5 10 15
155 gct aat cct gat aga ccc aac ttg aaa aag cgc 81
156 Ala Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg
157 20 25
160 <210> SEQ ID NO: 6
162 <211> LENGTH: 27
164 <212> TYPE: PRT
166 <213> ORGANISM: Schizosaccharomyces pombe
170 <400> SEQUENCE: 6
172 Lys Ser Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe
173 1 5 10 15

Input Set : A:\Sequence Listing (13111-00033-US).txt
Output Set: N:\CRF4\04062006\J572189.raw

176 Ala Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg
177 20 25
180 <210> SEQ ID NO: 7
182 <211> LENGTH: 78
184 <212> TYPE: DNA
186 <213> ORGANISM: Schizosaccharomyces pombe
190 <220> FEATURE:
192 <221> NAME/KEY: CDS
194 <222> LOCATION: (1)..(78)
198 <220> FEATURE:
200 <221> NAME/KEY: sig_peptide
202 <222> LOCATION: (1)..(60)
206 <400> SEQUENCE: 7
207 atg aag atc acc gct gtc att gcc ctt tta ttc tca ctt gct gct gcc 48
208 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
209 1 5 10 15
211 tca cct att cca gtt gcc gat cct ggt gtg 78
212 Ser Pro Ile Pro Val Ala Asp Pro Gly Val
213 20 25
216 <210> SEQ ID NO: 8
218 <211> LENGTH: 26
220 <212> TYPE: PRT
222 <213> ORGANISM: Schizosaccharomyces pombe
226 <400> SEQUENCE: 8
228 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
229 1 5 10 15
232 Ser Pro Ile Pro Val Ala Asp Pro Gly Val
233 20 25
236 <210> SEQ ID NO: 9
238 <211> LENGTH: 606
240 <212> TYPE: DNA
242 <213> ORGANISM: Schizosaccharomyces pombe
246 <220> FEATURE:
248 <221> NAME/KEY: CDS
250 <222> LOCATION: (1)..(606)
254 <400> SEQUENCE: 9
255 atg aag atc acc gct gtc att gcc ctt tta ttc tca ctt gct gct gcc 48
256 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
257 1 5 10 15
259 tca cct att cca gtt gcc gat cct ggt gtg gtt tca gtt agc aag tca 96
260 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
261 20 25 30
263 tat gct gat ttc ctt cgt gtt tac caa agt tgg aac act ttt gct aat 144
264 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
265 35 40 45
267 cct gat aga ccc aac ttg aaa aag cgc gaa ttc gaa gct gct ccc gca 192
268 Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala Pro Ala
269 50 55 60
271 aaa act tat gct gat ttc ctt cgt gct tat caa agt tgg aac act ttt 240

Input Set : A:\Sequence Listing (13111-00033-US).txt
Output Set: N:\CRF4\04062006\J572189.raw

272 Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser Trp Asn Thr Phe
273 65 70 75 80
275 gtt aat cct gac aga ccc aat ttg aaa aag cgt gag ttt gaa gct gcc 288
276 Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala
277 85 90 95
279 cca gag aag agt tat gct gat ttc ctt cgt gct tac cat agt tgg aac 336
280 Pro Glu Lys Ser Tyr Ala Asp Phe Leu Arg Ala Tyr His Ser Trp Asn
281 100 105 110
283 act ttt gtt aat cct gac aga ccc aac ttg aaa aag cgc gaa ttc gaa 384
284 Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu
285 115 120 125
287 gct gct ccc gca aaa act tat gct gat ttc ctt cgt gct tac caa agt 432
288 Ala Ala Pro Ala Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser
289 130 135 140
291 tgg aac act ttt gtt aat cct gac aga ccc aac ttg aaa aag cgc act 480
292 Trp Asn Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Thr
293 145 150 155 160
295 gaa gaa gat gaa gag aat gag gaa gag gat gaa gaa tac tat cgc ttt 528
296 Glu Glu Asp Glu Glu Asn Glu Glu Asp Glu Glu Tyr Tyr Arg Phe
297 165 170 175
299 ctt cag ttt tat atc atg act gtc cca gag aat tcc act att aca gat 576
300 Leu Gln Phe Tyr Ile Met Thr Val Pro Glu Asn Ser Thr Ile Thr Asp
301 180 185 190
303 gtc aat att act gcc aaa ttt gag agc taa 606
304 Val Asn Ile Thr Ala Lys Phe Glu Ser
305 195 200
308 <210> SEQ ID NO: 10
310 <211> LENGTH: 201
312 <212> TYPE: PRT
314 <213> ORGANISM: Schizosaccharomyces pombe
318 <400> SEQUENCE: 10
320 Met Lys Ile Thr Ala Val Ile Ala Leu Leu Phe Ser Leu Ala Ala Ala
321 1 5 10 15
324 Ser Pro Ile Pro Val Ala Asp Pro Gly Val Val Ser Val Ser Lys Ser
325 20 25 30
328 Tyr Ala Asp Phe Leu Arg Val Tyr Gln Ser Trp Asn Thr Phe Ala Asn
329 35 40 45
332 Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala Pro Ala
333 50 55 60
336 Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser Trp Asn Thr Phe
337 65 70 75 80
340 Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu Ala Ala
341 85 90 95
344 Pro Glu Lys Ser Tyr Ala Asp Phe Leu Arg Ala Tyr His Ser Trp Asn
345 100 105 110
348 Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Glu Phe Glu
349 115 120 125
352 Ala Ala Pro Ala Lys Thr Tyr Ala Asp Phe Leu Arg Ala Tyr Gln Ser
353 130 135 140

Input Set : A:\Sequence Listing (13111-00033-US).txt
Output Set: N:\CRF4\04062006\J572189.raw

356 Trp Asn Thr Phe Val Asn Pro Asp Arg Pro Asn Leu Lys Lys Arg Thr
357 145 150 155 160
360 Glu Glu Asp Glu Glu Asn Glu Glu Glu Asp Glu Glu Tyr Tyr Arg Phe
361 165 170 175
364 Leu Gln Phe Tyr Ile Met Thr Val Pro Glu Asn Ser Thr Ile Thr Asp
365 180 185 190
368 Val Asn Ile Thr Ala Lys Phe Glu Ser
369 195 200

372 <210> SEQ ID NO: 11
374 <211> LENGTH: 156
376 <212> TYPE: DNA
378 <213> ORGANISM: Unknown
382 <220> FEATURE:
384 <223> OTHER INFORMATION: to be completed

387 <220> FEATURE:
389 <221> NAME/KEY: CDS
391 <222> LOCATION: (1)...(156)
395 <400> SEQUENCE: 11

396 ctg gtt ccg cgt gga tcc atc gaa ggt cgt ggc ggc cgc atc ttt tac 48
397 Leu Val Pro Arg Gly Ser Ile Glu Gly Arg Gly Arg Ile Phe Tyr
398 1 5 10 15
400 cca tac gat gtt cct gac tat gcg ggc tat ccc tat gac gtc ccg gac 96
401 Pro Tyr Asp Val Pro Asp Tyr Ala Gly Tyr Pro Tyr Asp Val Pro Asp
402 20 25 30
404 tat gca gga tcc tat cca tat gac gtt cca gat tac gct gct cag tgc 144
405 Tyr Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala Gln Cys
406 35 40 45
408 ggc cgc taa tag 156
409 Gly Arg
410 50
413 <210> SEQ ID NO: 12
415 <211> LENGTH: 50
417 <212> TYPE: PRT
419 <213> ORGANISM: Unknown
423 <220> FEATURE:
425 <223> OTHER INFORMATION: to be completed

428 <400> SEQUENCE: 12

430 Leu Val Pro Arg Gly Ser Ile Glu Gly Arg Gly Arg Ile Phe Tyr
431 1 5 10 15
434 Pro Tyr Asp Val Pro Asp Tyr Ala Gly Tyr Pro Tyr Asp Val Pro Asp
435 20 25 30
438 Tyr Ala Gly Ser Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ala Gln Cys
439 35 40 45

442 Gly Arg
443 50
446 <210> SEQ ID NO: 13
448 <211> LENGTH: 354
450 <212> TYPE: DNA
452 <213> ORGANISM: Aspergillus nidulans

7 Invalid Response.
Explains the source of
genetic material.
See Item 11 on error
summary sheet.

Same Error

VERIFICATION SUMMARY
PATENT APPLICATION: US/10/572,189

DATE: 04/06/2006
TIME: 10:45:49

Input Set : A:\Sequence Listing (13111-00033-US).txt
Output Set: N:\CRF4\04062006\J572189.raw

::10 M:270 C: Current Application Number differs, Replaced Current Application No
::10 M:271 C: Current Filing Date differs, Replaced Current Filing Date